Amendments to the Claims:

This listing of the claims will replace all prior versions and listings of the claims in the application:

1–29. (Canceled)

30. (Previously Presented) A kit for quantifying the amount of a target moiety in a sample, the kit comprising a presentation system of claim 57.

31. (Withdrawn) (Currently Amended) A method of quantifying the amount of target moiety in a sample, the method comprising:

a) providing a presentation system of claim 57 ~~comprising at least one copy of the target moiety or part thereof that is recognizable by a binding partner and at least one domain which is non-reactive to said binding partner, said at least one copy of the target moiety being covalently bonded to the at least one domain of a scaffold material that has a controllable property~~;

b) carrying out a separation detection technique on said presentation system, wherein said presentation system is present in a specific amount;

c) generating at least one comparison point comprising an intensity of a signal produced by the presentation system versus the amount of the presentation system.

32. (Withdrawn) The method according to claim 31 wherein the presentation system is present in a single specific amount.

33. (Withdrawn) The method according to claim 31 wherein the presentation system is present in a series of varying amounts.

34. (Withdrawn) The method according to claim 33 wherein the varying amounts are in the same or different lanes or channels of a blot.

35. (Withdrawn) The method according to claim 33, wherein the comparison point

is a plurality of comparison points which together provide a calibration curve.

36. (Withdrawn) The method according to claim 31 further comprising comparing the comparison point or comparison points with the sample to quantify the amount of target moiety present in the sample.

37. (Withdrawn) The method according to claim 31, wherein said presentation system is of a known molecular weight or pI.

38. (Withdrawn) The method according to claim 31, wherein the presentation system comprises a non-biological polymer, a nucleic acid molecule, a peptide, protein or combinations thereof.

39. (Withdrawn) The method according to claim 31, wherein the presentation system comprises a plurality of domains linked in tandem.

40. (Withdrawn) The method according to claim 31, wherein the presentation system comprises identical units or domains or non-identical or different units or domains.

41. (Withdrawn) The method according to claim 31, wherein the unit(s) of the presentation system is/are non-reactive to the binding partner specific to the target moiety of part thereof.

42. (Withdrawn) The method according to claim 31, wherein the copy of the target moiety or part thereof comprises sequences of DNA, RNA, protein or peptide, saccharides, haptens, phosphate, nitrosylated groups, sulphated groups, GPI groups, an epitope, an antigenic structure or a chemical entity.

43. (Withdrawn) The method according to claim 42, wherein the copy of the target moiety comprises SERCA2a or SERCA2a phosphorylated on serine-38.

44. (Withdrawn) The method according to claim 31, wherein the presentation system comprises differing target moieties or parts thereof.

45. (Withdrawn) The method according to claim 31, wherein the copy of the target moiety or part thereof is linear or branched within the presentation system.

46. (Withdrawn) The method according to claim 31, wherein the specific binding partner comprises a molecule which has a specific binding affinity for the target moiety and is capable of binding thereto.

47. (Withdrawn) The method according to claim 46, wherein the binding partner comprises an antibody, DNA sequence, RNA sequence, a polypeptide, a dye, a metal chelate or a drug molecule.

48. (Withdrawn) The method according to claim 31, wherein the separation based detection technique comprises a dot blot, Western blot, RIA, fluorescence polarization, ELISA, Northern blotting, Southern blotting, PCR, High Performance Liquid Chromatography (HPLC), capillary electrophoresis, 1D electrophoresis, isoelectric focusing, mass spectrometry or combinations of the above.

49. (Withdrawn) The method according to claim 31, wherein the presentation system is a positive control for detecting the presence or absence of a target moiety in a sample.

50. (Withdrawn) The method according to claim 31, wherein the presentation system is an internal standard by providing a one point calibration.

51. (Withdrawn) The method according to claim 31, wherein the presentation system is used to generate multiple comparison points so as to provide a calibration curve.

52. (Withdrawn) The method according to claim 31, wherein the presentation system is used to monitor efficiency of immunoprecipitation and/or stages of an immunoprecipitation process.

53. (Canceled)

54. (Withdrawn)(Currently Amended) A method for quantifying an amount of a protein epitope in a sample, said method comprising:

(a) providing a protein presentation system of claim 57 ~~comprising at least one copy of the protein epitope and at least one further protein domain, wherein said presentation system is of known molecular weight~~;

b) carrying out a Western blot experiment on said presentation system, wherein said presentation system is in a specific concentration; wherein said Western blot experiment utilizes a binding partner specific to the target moiety; and further wherein said protein domain of the presentation system is non-reactive to the binding partner; and

c) generating a comparison point comprising an intensity of a signal produced by the presentation system in said technique compared to the concentration of the presentation system.

55-56. (Canceled)

57. (Currently Amended) A non-natural presentation system, comprising at least one copy of a target moiety or part thereof that is recognizable by a binding partner and at least one domain of a scaffold material covalently linked to said target moiety wherein the scaffold material has a controllable property selected from the group consisting of:

(i) molecular weight;

(ii) isoelectric point;

(iii) number of chemically reactive cysteine amino acid residues;

(iv) number of chemically reactive lysine amino acid residues; and

(v) an affinity purification feature,

~~and~~ wherein the at least one domain of the scaffold is non-reactive to a binding partner specific to said target moiety or part thereof.